

SEQUENCE LISTING

<110> Digan, Mary Ellen
Lake, Philip
Wright, Richard M.

<120> Anti-CD3 Immunotoxins and Therapeutic Uses Therefor

<130> CGC 4-31157A/USN

<140> 09/---,---

<141> 2000-01-10

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 601

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
scFv(UCHT-1)-PE38 amino acid sequence

<400> 1

Met	Ala	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	Ser
1				5					10					15	

Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	Arg
		20						25					30		

Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	Leu
		35					40					45			

Leu	Ile	Tyr	Tyr	Thr	Ser	Arg	Leu	His	Ser	Gly	Val	Pro	Ser	Lys	Phe
	50					55					60				

Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	Leu
65					70					75				80	

Glu	Gln	Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	Leu
				85					90					95	

Pro	Trp	Thr	Phe	Ala	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Ala	Gly
				100				105						110	

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Glu	115	120	125
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser	130	135	140
Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr	145	150	155
Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met Gly	165	170	175
Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys	180	185	190
Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met	195	200	205
Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala	210	215	220
Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly	225	230	235
Ala Gly Thr Thr Val Thr Val Ser Ser Lys Ala Ser Gly Gly Pro Glu	245	250	255
Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro	260	265	270
Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu	275	280	285
Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala	290	295	300
Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu	305	310	315
Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln	325	330	335
Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu	340	345	350
Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn	355	360	365

Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr
 370 375 380

Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg
 385 390 395 400

Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln
 405 410 415

Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu
 420 425 430

Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln
 435 440 445

Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala
 450 455 460

Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg
 465 470 475 480

Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu
 485 490 495

Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala
 500 505 510

Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp
 515 520 525

Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu
 530 535 540

Gly Trp Pro Leu Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro
 545 550 555 560

Thr Asp Pro Arg Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro
 565 570 575

Asp Lys Glu Gln Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro
 580 585 590

Gly Lys Pro Pro Arg Glu Asp Leu Lys
 595 600

<210> 2

<211> 1803

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence:
 scFv(UCHT-1)-PE38 nucleotide sequence

<220>
 <221> misc_feature
 <222> (1)..(6)
 <223> NcoI restriction site

<220>
 <221> misc_feature
 <222> (336)..(383)
 <223> linker

<220>
 <221> misc_feature
 <222> (751)..(756)
 <223> HindIII restriction site

<400> 2
 atggcgagaca tccagatgac ccagaccacc tcctccctgt ctgcctctct gggagacaga 60
 gtcaccatca gttgcagggc aagtcaggac attagaaatt atttaaactg gtatcaacag 120
 aaaccagatg gaactgttaa actcctgac tactacacat caagattaca ctccaggagtc 180
 ccatcaaagt tcagtggcag tgggtctgga acagattatt ctctcaccat tagcaacctg 240
 gagcaagagg atattgccac ttacttttgc caacagggta atacgcttcc gtggacgttc 300
 gctggaggca ccaagctgga aatcaaaccg gctggaggcg gtagtggcgg tggatcgggt 360
 ggaggcagcg gtggcggatc tgaggtgcag ctccagcagt ctggacctga gctgggtgaag 420
 cctggagctt caatgaagat atcctgcaag gcttctgggt actcattcac tggctacacc 480
 atgaactggg tgaagcagag tcatggaaag aaccttgagt ggatgggact tattaatcct 540
 taaaagggtg ttagtaccta caaccagaag ttcaaggaca aggccacatt aactgtagac 600
 aagtcattca gcacagccta catggaactc ctcagtctga catctgagga ctctgcagtc 660
 tattactgtg caagatcggg gtactacggg gatagtgact ggtacttcga tgtctggggc 720
 gcagggacca cggtcaccgt ctcccaaaa gcttcggag gtcccgagg cggcagcctg 780
 gccgcgctga ccgcgcacca ggcttgccac ctgccgctgg agaatttcac ccgtcatcgc 840
 cagccgcgcg gctgggaaca actggagcag tgcggctatc cgggtgcagcg gctgggtcgcc 900
 ctctacctgg cggcgcggtg gtcgtggaac caggctgacc aggtgatccg caacgccttg 960
 gccagccccg gcagcggcgg cgacctgggc gaagcgatcc gcgagcagcc ggagcaggcc 1020
 cgtctggccc tgacctggc cgccgcgag agcgagcgt tcgtccggca gggcaccggc 1080
 aacgacgagg ccggcgcgcc caacggcccc gcgagcagcg gcgacgcctt gctggagcgc 1140
 aactatccca ctggcgcgga gttcctcggc gacggcgggc acgtcagctt cagcaccgcg 1200
 ggcacgcaga actggacggg ggagcggctg ctccaggcgc accgccaact ggaggagcgc 1260
 ggctatgtgt tcgtcggtc ccacggcacc ttctcgaag cggcgcaaag catcgtcttc 1320
 ggcggggtgc gcgcgcgag ccaggacctc gacgcgatct ggcgcggttt ctatatcgcc 1380
 ggcgatccgg cgctggccta cggctacgcc caggaccagg aaccgcagcg acgcggcccg 1440
 atccgcaacg gtgccctgct gcgggtctat gtgccgcgct cgagcctgcc gggcttctac 1500

cgcaccagcc tgaccctggc cgcgccggag gcggcgggcg aggtcgaacg gctgatcggc 1560
 catccgctgc cgctgcgcct ggacgccatc accggccccg aggaggaagg cgggcgcctg 1620
 gagaccattc tcggctggcc gctggccgag cgcaccgtgg tgattccctc ggcgatcccc 1680
 accgaccgcg gcaacgtcgg cggcgacctc gacccgtcca gcatccccga caaggaacag 1740
 gcgatcagcg ccctgccgga ctacgccagc cagcccggca aaccgccgcg cgaggacctg 1800
 aag 1803

<210> 3

<211> 613

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 3

Ala Glu Glu Ala Phe Asp Leu Trp Asn Glu Cys Ala Lys Ala Cys Val
 1 5 10 15

Leu Asp Leu Lys Asp Gly Val Arg Ser Ser Arg Met Ser Val Asp Pro
 20 25 30

Ala Ile Ala Asp Thr Asn Gly Gln Gly Val Leu His Tyr Ser Met Val
 35 40 45

Leu Glu Gly Gly Asn Asp Ala Leu Lys Leu Ala Ile Asp Asn Ala Leu
 50 55 60

Ser Ile Thr Ser Asp Gly Leu Thr Ile Arg Leu Glu Gly Gly Val Glu
 65 70 75 80

Pro Asn Lys Pro Val Arg Tyr Ser Tyr Thr Arg Gln Ala Arg Gly Ser
 85 90 95

Trp Ser Leu Asn Trp Leu Val Pro Ile Gly His Glu Lys Pro Ser Asn
 100 105 110

Ile Lys Val Phe Ile His Glu Leu Asn Ala Gly Asn Gln Leu Ser His
 115 120 125

Met Ser Pro Ile Tyr Thr Ile Glu Met Gly Asp Glu Leu Leu Ala Lys
 130 135 140

Leu Ala Arg Asp Ala Thr Phe Phe Val Arg Ala His Glu Ser Asn Glu
 145 150 155 160

Met Gln Pro Thr Leu Ala Ile Ser His Ala Gly Val Ser Val Val Met
 165 170 175

Ala Gln Thr Gln Pro Arg Arg Glu Lys Arg Trp Ser Glu Trp Ala Ser
 180 185 190

Gly Lys Val Leu Cys Leu Leu Asp Pro Leu Asp Gly Val Tyr Asn Tyr
 195 200 205

Leu Ala Gln Gln Arg Cys Asn Leu Asp Asp Thr Trp Glu Gly Lys Ile
 210 215 220

Tyr Arg Val Leu Ala Gly Asn Pro Ala Lys His Asp Leu Asp Ile Lys
 225 230 235 240

Pro Thr Val Ile Ser His Arg Leu His Phe Pro Glu Gly Gly Ser Leu
 245 250 255

Ala Ala Leu Thr Ala His Gln Ala Cys His Leu Pro Leu Glu Thr Phe
 260 265 270

Thr Arg His Arg Gln Pro Arg Gly Trp Glu Gln Leu Glu Gln Cys Gly
 275 280 285

Tyr Pro Val Gln Arg Leu Val Ala Leu Tyr Leu Ala Ala Arg Leu Ser
 290 295 300

Trp Asn Gln Val Asp Gln Val Ile Arg Asn Ala Leu Ala Ser Pro Gly
 305 310 315 320

Ser Gly Gly Asp Leu Gly Glu Ala Ile Arg Glu Gln Pro Glu Gln Ala
 325 330 335

Arg Leu Ala Leu Thr Leu Ala Ala Ala Glu Ser Glu Arg Phe Val Arg
 340 345 350

Gln Gly Thr Gly Asn Asp Glu Ala Gly Ala Ala Asn Ala Asp Val Val
 355 360 365

Ser Leu Thr Cys Pro Val Ala Ala Gly Glu Cys Ala Gly Pro Ala Asp
 370 375 380

Ser Gly Asp Ala Leu Leu Glu Arg Asn Tyr Pro Thr Gly Ala Glu Phe
 385 390 395 400

Leu Gly Asp Gly Gly Asp Val Ser Phe Ser Thr Arg Gly Thr Gln Asn
 405 410 415

Trp Thr Val Glu Arg Leu Leu Gln Ala His Arg Gln Leu Glu Glu Arg
 420 425 430

Gly Tyr Val Phe Val Gly Tyr His Gly Thr Phe Leu Glu Ala Ala Gln
 435 440 445

Ser Ile Val Phe Gly Gly Val Arg Ala Arg Ser Gln Asp Leu Asp Ala
 450 455 460

Ile Trp Arg Gly Phe Tyr Ile Ala Gly Asp Pro Ala Leu Ala Tyr Gly
 465 470 475 480

Tyr Ala Gln Asp Gln Glu Pro Asp Ala Arg Gly Arg Ile Arg Asn Gly
 485 490 495

Ala Leu Leu Arg Val Tyr Val Pro Arg Ser Ser Leu Pro Gly Phe Tyr
 500 505 510

Arg Thr Ser Leu Thr Leu Ala Ala Pro Glu Ala Ala Gly Glu Val Glu
 515 520 525

Arg Leu Ile Gly His Pro Leu Pro Leu Arg Leu Asp Ala Ile Thr Gly
 530 535 540

Pro Glu Glu Glu Gly Gly Arg Leu Glu Thr Ile Leu Gly Trp Pro Leu
 545 550 555 560

Ala Glu Arg Thr Val Val Ile Pro Ser Ala Ile Pro Thr Asp Pro Arg
 565 570 575

Asn Val Gly Gly Asp Leu Asp Pro Ser Ser Ile Pro Asp Lys Glu Gln
 580 585 590

Ala Ile Ser Ala Leu Pro Asp Tyr Ala Ser Gln Pro Gly Lys Pro Pro
 595 600 605

Arg Glu Asp Leu Lys
 610

<210> 4

<211> 25

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 4

Met His Leu Ile Pro His Trp Ile Pro Leu Val Ala Ser Leu Gly Leu
 1 5 10 15

Leu Ala Gly Gly Ser Ser Ala Ser Ala
 20 25

<210> 5
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker

<400> 5
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PE peptide

<400> 6
Arg Glu Asp Leu Lys
1 5

<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PE peptide

<400> 7
Arg Glu Asp Leu
1

<210> 8
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PE peptide

<400> 8

Lys Asp Glu Leu

1

<210> 9

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide
connector

<400> 9

Lys Ala Ser Gly Gly

1

5

<210> 10

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide linker

<400> 10

Gly Gly Gly Gly Ser

1

5

<210> 11

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer IM-34A

<400> 11

gcggatccga catccagatg acccagacca cc

32

<210> 12

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer IM-34B

<400> 12
cctctagaag cccgtttgat ttccagcttg gt 32

<210> 13
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer IM-34C

<400> 13
ccaagctttc atgaggagac ggtgaccgtg gtccc 35

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer IM-61

<400> 14
ccgtcgacga ggtgcagctc cagcagtct 29

<210> 15
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligo IM24A

<400> 15
ctagaggagg tagtggaggc tcaggagggtt ctggaggtag tg 42

<210> 16
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer IM-24B

<400> 16
tcgacactac ctccagaacc tcctgagcct ccactacctc ct 42

<210> 17
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer VL1

<400> 17
ctggtatcaa cagaaaccag atc 23

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer VL2

<400> 18
ggtgcctcca gcgaacgtcc acggaag 27

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer VL3

<400> 19
cttccgtgga cgttcgctgg aggcacc 27

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer VH4

<400> 20
ctctgcttca cccagttcat g 21

<210> 21
<211> 66
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer VL6

<400> 21

gccaccgctg cctccacctg atccaccgcc actaccgcct ccagcccgtt tgatttccag 60
cttggt 66

<210> 22

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer VL8

<400> 22

tcaggtccag actgctggag ctgcacctca gatccgccac cgctgcctcc acctgat 57